Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 06:12 PM EDT

PDB ID	:	3IG4
Title	:	Structure of a putative aminopeptidase P from Bacillus anthracis
Authors	:	Anderson, S.M.; Wawrzak, Z.; Skarina, T.; Onopriyenko, O.; Kwon, K.; Anderson, W.F.; Savchenko, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2009-07-27
Resolution	:	2.89 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

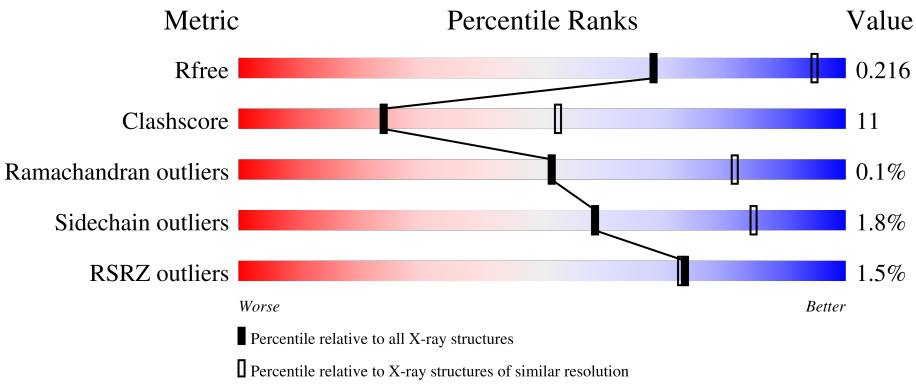
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	427	% 81% 17% •
1	B	427	78% 20% •
1	C	427	% 80% 18% • •
1	D	427	78% 19% • •
1	E	427	5% 74% 23% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	427	2% 77% 20%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	430	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 20528 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

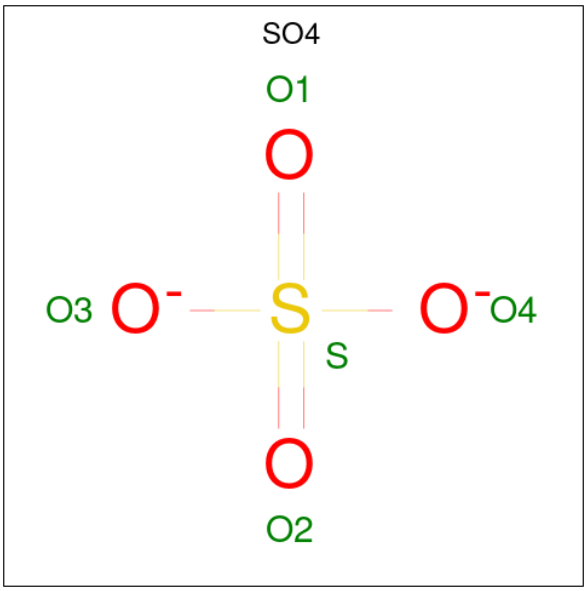
- Molecule 1 is a protein called Xaa-pro aminopeptidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	419	3385	2162	553	658	3	9	0	1	0
1	B	419	3385	2162	553	658	3	9	0	1	0
1	C	419	3385	2162	553	658	3	9	0	1	0
1	D	419	3390	2165	554	659	3	9	0	2	0
1	E	419	3385	2162	553	658	3	9	0	1	0
1	F	419	3391	2167	554	658	3	9	0	2	0

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
2	A	2	2	2	0	0
2	B	2	2	2	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0
2	E	2	2	2	0	0
2	F	2	2	2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	A	1	10	8	2		0	1
			Total	O	S			
3	A	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0
			Total	O	S			
3	B	1	5	4	1		0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	C	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	D	1	5	4	1		0	0
			Total	O	S			
3	E	1	5	4	1		0	0
			Total	O	S			
3	E	1	5	4	1		0	0
			Total	O	S			
3	E	1	5	4	1		0	0
			Total	O	S			
3	E	1	5	4	1		0	0
			Total	O	S			
3	E	1	5	4	1		0	0
			Total	O	S			
3	F	1	5	4	1		0	0
			Total	O	S			
3	F	1	5	4	1		0	0
			Total	O	S			
3	F	1	5	4	1		0	0

Continued on next page...

Continued from previous page...

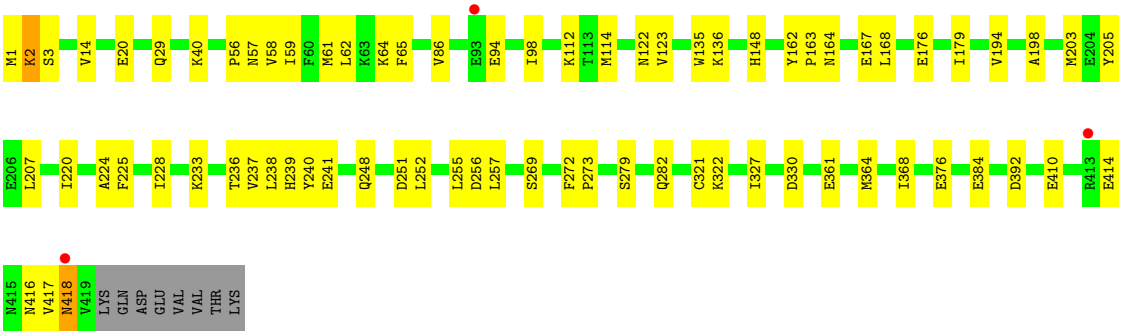
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	F	1	5	4	1	0	0
			Total	O	S		
3	F	1	5	4	1	0	0
			Total	O	S		
3	F	1	5	4	1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

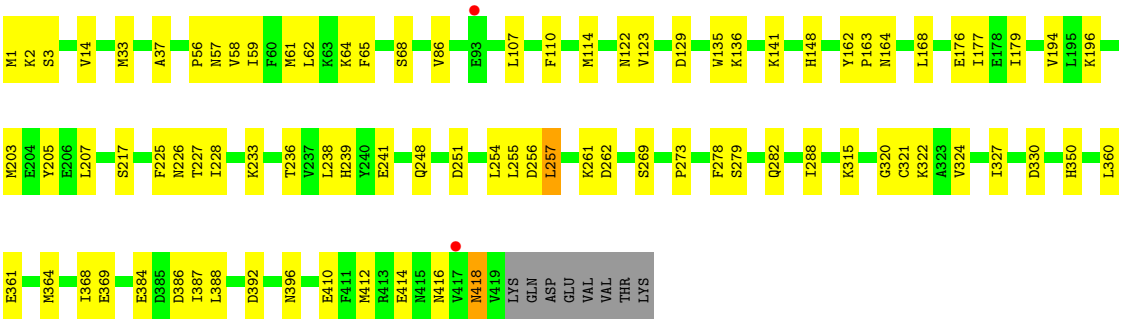
• Molecule 1: Xaa-pro aminopeptidase

Chain A:



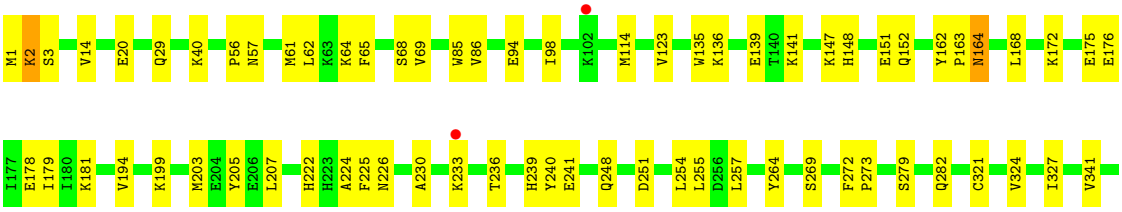
• Molecule 1: Xaa-pro aminopeptidase

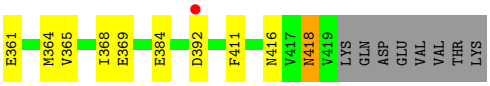
Chain B:



• Molecule 1: Xaa-pro aminopeptidase

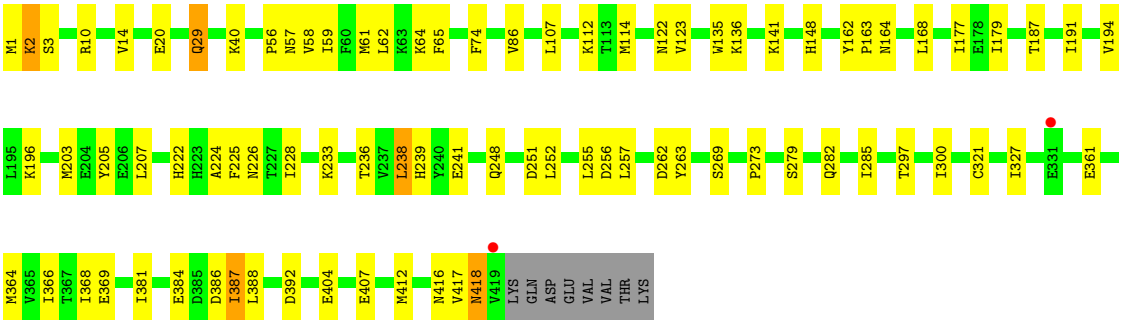
Chain C:





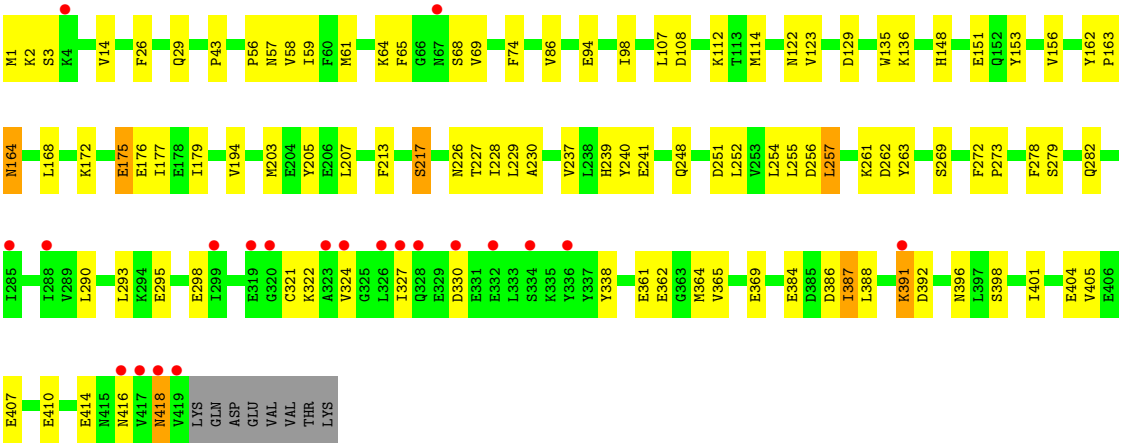
• Molecule 1: Xaa-pro aminopeptidase

Chain D:



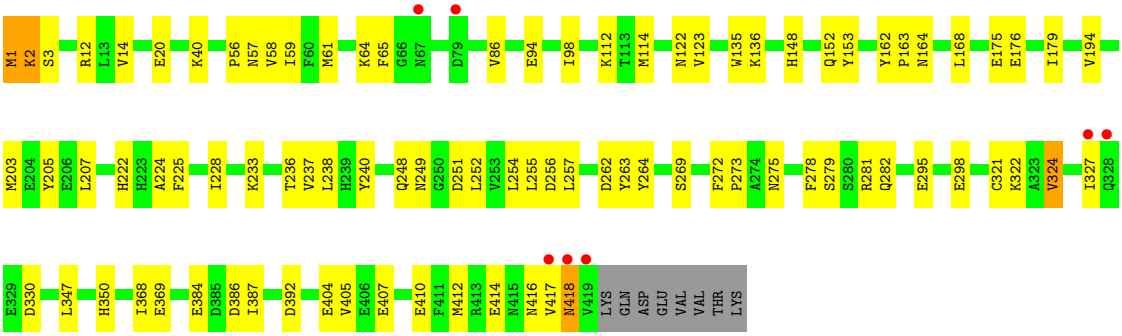
• Molecule 1: Xaa-pro aminopeptidase

Chain E:



• Molecule 1: Xaa-pro aminopeptidase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	180.88Å 180.88Å 254.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.40 – 2.89 44.39 – 2.89	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.40-2.89) 99.6 (44.39-2.89)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.49 (at 2.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.198 , 0.226 0.193 , 0.216	Depositor DCC
R_{free} test set	4743 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	67.2	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 30.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	20528	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.44	0/3447	0.51	0/4641
1	B	0.47	0/3447	0.52	0/4641
1	C	0.43	0/3447	0.50	0/4641
1	D	0.47	0/3455	0.52	0/4652
1	E	0.43	0/3447	0.49	0/4641
1	F	0.45	0/3456	0.50	0/4652
All	All	0.45	0/20699	0.51	0/27868

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3385	0	3336	71	0
1	B	3385	0	3336	80	0
1	C	3385	0	3336	76	0
1	D	3390	0	3342	92	0
1	E	3385	0	3336	93	0
1	F	3391	0	3349	82	0
2	A	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	45	0	0	3	0
3	B	30	0	0	2	0
3	C	30	0	0	1	0
3	D	35	0	0	2	0
3	E	25	0	0	0	0
3	F	30	0	0	2	0
All	All	20528	0	20035	449	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (449) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1:MSE:HE2	1:D:179:ILE:HD12	1.32	1.11
1:A:61:MSE:CE	1:A:114:MSE:HE1	1.82	1.08
1:D:61:MSE:CE	1:D:114:MSE:HE1	1.86	1.04
1:F:61:MSE:CE	1:F:114:MSE:HE1	1.87	1.04
1:A:61:MSE:HE1	1:A:114:MSE:CE	1.89	1.03
1:B:61:MSE:CE	1:B:114:MSE:HE1	1.89	1.01
1:D:61:MSE:HE1	1:D:114:MSE:CE	1.90	1.01
1:E:61:MSE:CE	1:E:114:MSE:HE1	1.90	1.00
1:C:61:MSE:HE1	1:C:114:MSE:CE	1.94	0.97
1:B:279:SER:H	1:B:282:GLN:HE21	1.11	0.97
1:F:61:MSE:HE1	1:F:114:MSE:CE	1.96	0.96
1:C:61:MSE:CE	1:C:114:MSE:HE1	1.97	0.95
1:C:2:LYS:HD3	1:C:3:SER:H	1.27	0.95
1:C:1:MSE:HE2	1:C:179:ILE:HD12	1.48	0.94
1:D:1:MSE:HE2	1:D:179:ILE:CD1	1.98	0.94
1:F:61:MSE:HE2	1:F:114:MSE:HE1	1.46	0.94
1:F:56:PRO:HB2	1:F:57:ASN:HD22	1.32	0.93
1:F:1:MSE:HE2	1:F:179:ILE:HD12	1.50	0.93
1:D:29:GLN:NE2	1:D:141:LYS:HD2	1.83	0.92
1:A:61:MSE:HE2	1:A:114:MSE:HE1	1.52	0.92
1:C:2:LYS:HD3	1:C:3:SER:N	1.84	0.91
1:E:61:MSE:HE1	1:E:114:MSE:HE1	1.50	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:56:PRO:HB2	1:F:57:ASN:ND2	1.85	0.90
1:B:61:MSE:HE2	1:B:114:MSE:HE1	1.53	0.90
1:C:40:LYS:HE3	1:D:226:ASN:HD21	1.38	0.89
1:D:279:SER:H	1:D:282:GLN:HE21	1.19	0.89
1:A:65:PHE:HZ	1:A:123:VAL:HG22	1.37	0.89
1:A:1:MSE:HE2	1:A:179:ILE:HD12	1.53	0.88
1:D:61:MSE:HE1	1:D:114:MSE:HE1	1.45	0.87
1:C:279:SER:H	1:C:282:GLN:HE21	1.19	0.87
1:E:2:LYS:HD3	1:E:3:SER:N	1.90	0.86
1:B:61:MSE:HE1	1:B:114:MSE:CE	2.05	0.85
1:E:279:SER:H	1:E:282:GLN:HE21	1.22	0.85
1:E:362:GLU:OE2	1:E:391:LYS:HG2	1.75	0.85
1:F:61:MSE:CE	1:F:114:MSE:CE	2.52	0.84
1:A:279:SER:H	1:A:282:GLN:HE21	1.24	0.84
1:B:2:LYS:HD3	1:B:3:SER:N	1.92	0.83
1:C:61:MSE:HE1	1:C:114:MSE:HE1	1.57	0.83
1:D:2:LYS:HD3	1:D:3:SER:H	1.44	0.81
1:B:61:MSE:CE	1:B:114:MSE:CE	2.58	0.81
1:D:279:SER:H	1:D:282:GLN:NE2	1.78	0.81
1:A:61:MSE:HE1	1:A:114:MSE:HE1	1.49	0.80
1:D:61:MSE:HE2	1:D:114:MSE:HE1	1.64	0.80
1:A:65:PHE:CZ	1:A:123:VAL:HG22	2.16	0.79
1:E:2:LYS:HD3	1:E:3:SER:H	1.44	0.79
1:E:61:MSE:HE1	1:E:114:MSE:CE	2.12	0.78
1:B:2:LYS:HD3	1:B:3:SER:H	1.48	0.78
1:B:61:MSE:HE1	1:B:114:MSE:HE1	1.65	0.77
1:E:164:ASN:H	1:E:164:ASN:HD22	1.30	0.77
1:A:61:MSE:CE	1:A:114:MSE:CE	2.52	0.77
1:D:2:LYS:HD3	1:D:3:SER:N	1.99	0.76
1:D:29:GLN:HE22	1:D:141:LYS:HD2	1.48	0.76
1:E:65:PHE:HZ	1:E:123:VAL:HG22	1.51	0.76
1:F:2:LYS:HD3	1:F:3:SER:N	2.02	0.75
1:D:56:PRO:O	1:D:57:ASN:HB2	1.86	0.75
1:A:2:LYS:HD3	1:A:3:SER:N	2.01	0.75
1:E:321:CYS:HB3	1:E:327:ILE:HG12	1.68	0.75
1:F:164:ASN:O	1:F:168:LEU:HD12	1.86	0.75
1:C:61:MSE:HE2	1:C:114:MSE:HE1	1.68	0.74
1:A:164:ASN:HD22	1:A:164:ASN:H	1.36	0.74
1:D:164:ASN:O	1:D:168:LEU:HD13	1.86	0.74
1:B:164:ASN:H	1:B:164:ASN:HD22	1.36	0.74
1:C:1:MSE:HE2	1:C:179:ILE:CD1	2.17	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:164:ASN:HD22	1:C:164:ASN:H	1.34	0.73
1:C:14:VAL:HG13	1:C:64:LYS:HE3	1.71	0.72
1:B:279:SER:H	1:B:282:GLN:NE2	1.85	0.72
1:D:148:HIS:HD2	1:F:135:TRP:CH2	2.06	0.72
1:C:222:HIS:HA	3:C:433:SO4:O2	1.89	0.72
1:C:61:MSE:CE	1:C:114:MSE:CE	2.63	0.71
1:C:279:SER:H	1:C:282:GLN:NE2	1.88	0.71
1:E:61:MSE:HE2	1:E:114:MSE:HE1	1.72	0.71
1:F:65:PHE:HZ	1:F:123:VAL:HG22	1.53	0.71
1:C:29:GLN:HE22	1:C:141:LYS:HD2	1.57	0.70
1:A:162:TYR:HB3	1:A:163:PRO:HD3	1.72	0.70
1:B:14:VAL:HG13	1:B:64:LYS:HE3	1.72	0.70
1:B:162:TYR:HB3	1:B:163:PRO:HD3	1.74	0.69
1:F:65:PHE:CZ	1:F:123:VAL:HG22	2.27	0.69
1:F:279:SER:H	1:F:282:GLN:HE21	1.41	0.69
1:A:135:TRP:CH2	1:C:148:HIS:HD2	2.11	0.68
1:F:321:CYS:HB3	1:F:327:ILE:HG12	1.75	0.68
1:F:203:MSE:HG2	1:F:205:TYR:CZ	2.29	0.68
1:E:387:ILE:HD13	1:E:387:ILE:N	2.08	0.67
1:F:61:MSE:HE1	1:F:114:MSE:HE1	1.63	0.67
1:E:14:VAL:HG13	1:E:64:LYS:HE3	1.77	0.67
1:B:65:PHE:HZ	1:B:123:VAL:HG22	1.60	0.67
1:E:65:PHE:CZ	1:E:123:VAL:HG22	2.30	0.67
1:A:2:LYS:HD3	1:A:3:SER:H	1.59	0.67
1:C:162:TYR:HB3	1:C:163:PRO:HD3	1.77	0.66
1:B:203:MSE:HG2	1:B:205:TYR:CZ	2.31	0.66
1:D:61:MSE:CE	1:D:114:MSE:CE	2.58	0.66
1:A:1:MSE:HE2	1:A:179:ILE:CD1	2.24	0.66
1:F:369:GLU:HB3	1:F:384:GLU:HB2	1.78	0.66
1:C:65:PHE:HZ	1:C:123:VAL:HG22	1.60	0.65
1:E:239:HIS:O	1:E:241:GLU:HG3	1.96	0.65
1:D:194:VAL:HG13	1:D:207:LEU:HD22	1.77	0.65
1:F:279:SER:H	1:F:282:GLN:NE2	1.94	0.65
1:B:254:LEU:C	1:B:254:LEU:HD23	2.17	0.65
1:D:387:ILE:HD13	1:D:387:ILE:N	2.12	0.65
1:D:203:MSE:HG2	1:D:205:TYR:CZ	2.32	0.65
1:A:135:TRP:CZ2	1:C:148:HIS:HD2	2.15	0.64
1:C:164:ASN:O	1:C:168:LEU:HD13	1.97	0.64
1:B:148:HIS:HD2	1:D:135:TRP:CH2	2.16	0.64
1:E:254:LEU:HD23	1:E:254:LEU:C	2.19	0.63
1:D:164:ASN:O	1:D:168:LEU:CD1	2.46	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:416:ASN:OD1	1:E:418:ASN:ND2	2.31	0.63
1:B:65:PHE:CZ	1:B:123:VAL:HG22	2.32	0.63
1:A:29:GLN:OE1	1:A:57:ASN:ND2	2.32	0.63
1:D:228:ILE:HB	1:D:256:ASP:HB3	1.81	0.62
1:A:14:VAL:O	1:A:64:LYS:HE3	2.00	0.62
1:C:40:LYS:CE	1:D:226:ASN:HD21	2.09	0.62
1:A:136:LYS:NZ	1:D:136:LYS:NZ	2.46	0.62
1:D:162:TYR:HB3	1:D:163:PRO:HD3	1.82	0.62
1:F:1:MSE:HE2	1:F:179:ILE:CD1	2.25	0.62
1:A:1:MSE:CE	1:A:179:ILE:HD12	2.30	0.61
1:B:56:PRO:O	1:B:57:ASN:HB2	1.99	0.61
1:A:279:SER:H	1:A:282:GLN:NE2	1.95	0.61
1:F:350:HIS:NE2	3:F:430:SO4:O2	2.33	0.61
1:D:418:ASN:ND2	1:D:418:ASN:H	1.99	0.61
1:D:65:PHE:HZ	1:D:123:VAL:HG22	1.66	0.61
1:A:136:LYS:HZ1	1:D:136:LYS:HZ2	1.46	0.60
1:A:269:SER:H	1:A:384:GLU:HB3	1.67	0.60
1:D:29:GLN:HE22	1:D:141:LYS:CD	2.15	0.60
1:D:361:GLU:HB2	1:D:364:MSE:HE3	1.84	0.60
1:A:136:LYS:HZ3	1:D:136:LYS:HZ1	1.48	0.59
1:B:324:VAL:CG1	1:B:324:VAL:O	2.50	0.59
1:B:416:ASN:OD1	1:B:418:ASN:ND2	2.35	0.59
1:E:86:VAL:HG12	1:E:86:VAL:O	2.01	0.59
1:D:29:GLN:NE2	1:D:141:LYS:CD	2.64	0.59
1:F:222:HIS:ND1	3:F:433:SO4:O4	2.30	0.59
1:F:61:MSE:HE1	1:F:114:MSE:HE3	1.84	0.58
1:E:237:VAL:HB	1:E:240:TYR:HB2	1.85	0.58
1:A:135:TRP:CZ2	1:C:148:HIS:CD2	2.91	0.58
1:A:248:GLN:O	1:A:251:ASP:HB2	2.04	0.58
1:A:416:ASN:OD1	1:A:418:ASN:ND2	2.36	0.58
1:F:228:ILE:HB	1:F:256:ASP:HB3	1.86	0.58
1:B:14:VAL:CG1	1:B:64:LYS:HE3	2.33	0.58
1:F:12:ARG:HB3	1:F:168:LEU:HD21	1.85	0.58
1:E:272:PHE:HB2	1:E:273:PRO:HD2	1.84	0.58
1:C:61:MSE:HE1	1:C:114:MSE:HE3	1.86	0.57
1:A:14:VAL:HG13	1:A:64:LYS:HE2	1.87	0.57
1:E:94:GLU:O	1:E:98:ILE:HG13	2.04	0.57
1:B:1:MSE:HE2	1:B:179:ILE:HD12	1.86	0.57
1:A:252:LEU:HD12	1:A:273:PRO:HA	1.87	0.57
1:E:228:ILE:HB	1:E:256:ASP:HB3	1.86	0.57
1:A:225:PHE:CE2	3:A:430:SO4:O4	2.58	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:MSE:HE2	1:B:179:ILE:CD1	2.35	0.57
1:C:361:GLU:HB2	1:C:364:MSE:HE3	1.86	0.57
1:D:164:ASN:H	1:D:164:ASN:HD22	1.52	0.57
1:D:386:ASP:C	1:D:387:ILE:HD13	2.25	0.57
1:E:279:SER:H	1:E:282:GLN:NE2	1.97	0.57
1:E:172:LYS:HG3	1:E:365:VAL:HG23	1.86	0.56
1:F:162:TYR:HB3	1:F:163:PRO:HD3	1.87	0.56
1:E:361:GLU:HB2	1:E:364:MSE:HE3	1.87	0.56
1:F:2:LYS:HD3	1:F:3:SER:H	1.70	0.56
1:A:361:GLU:HB2	1:A:364:MSE:HE3	1.87	0.56
1:C:203:MSE:HG2	1:C:205:TYR:CZ	2.41	0.56
1:B:369:GLU:HB3	1:B:384:GLU:HG3	1.88	0.56
1:E:203:MSE:HG2	1:E:205:TYR:CZ	2.40	0.56
1:F:416:ASN:OD1	1:F:418:ASN:ND2	2.39	0.56
1:E:162:TYR:HB3	1:E:163:PRO:HD3	1.87	0.56
1:A:94:GLU:O	1:A:98:ILE:HG13	2.06	0.55
1:A:228:ILE:HB	1:A:256:ASP:HB3	1.87	0.55
1:B:273:PRO:HD3	1:B:278:PHE:CE2	2.41	0.55
1:E:86:VAL:O	1:E:86:VAL:CG1	2.53	0.55
1:E:164:ASN:O	1:E:168:LEU:HD13	2.06	0.55
1:A:225:PHE:CD2	3:A:430:SO4:O4	2.60	0.55
1:C:65:PHE:CZ	1:C:123:VAL:HG22	2.41	0.55
1:A:248:GLN:HA	1:A:248:GLN:NE2	2.22	0.55
1:F:14:VAL:HG13	1:F:64:LYS:HE3	1.89	0.55
1:F:233:LYS:O	1:F:236:THR:HB	2.07	0.55
1:E:404:GLU:HB2	1:E:407:GLU:HG3	1.88	0.54
1:F:322:LYS:NZ	1:F:330:ASP:OD1	2.26	0.54
1:F:392:ASP:OD1	1:F:392:ASP:N	2.40	0.54
1:C:226:ASN:HD21	1:D:40:LYS:HE2	1.72	0.54
1:D:29:GLN:OE1	1:D:57:ASN:OD1	2.26	0.54
1:D:239:HIS:O	1:D:241:GLU:HG3	2.08	0.54
1:C:194:VAL:HG13	1:C:207:LEU:HD22	1.89	0.54
1:E:252:LEU:HD12	1:E:273:PRO:HA	1.89	0.54
1:A:272:PHE:HB2	1:A:273:PRO:HD2	1.90	0.54
1:A:164:ASN:O	1:A:168:LEU:HD13	2.08	0.53
1:B:410:GLU:OE2	1:B:414:GLU:OE1	2.27	0.53
1:A:148:HIS:HD2	1:E:135:TRP:CH2	2.26	0.53
1:E:269:SER:H	1:E:384:GLU:HB3	1.74	0.53
1:E:418:ASN:ND2	1:E:418:ASN:H	2.06	0.53
1:C:392:ASP:OD1	1:C:392:ASP:N	2.38	0.53
1:D:20:GLU:HA	1:D:65:PHE:CD1	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ALA:HA	1:A:207:LEU:HD21	1.91	0.53
1:F:20:GLU:HA	1:F:65:PHE:CD1	2.43	0.53
1:C:239:HIS:O	1:C:241:GLU:HG3	2.08	0.53
1:D:65:PHE:CZ	1:D:123:VAL:HG22	2.43	0.53
1:E:43:PRO:HG2	1:E:263:TYR:CE1	2.44	0.53
1:A:220:ILE:O	1:A:220:ILE:HG22	2.09	0.52
1:B:361:GLU:HB2	1:B:364:MSE:HE3	1.91	0.52
1:F:12:ARG:HB3	1:F:168:LEU:CD2	2.39	0.52
1:A:239:HIS:O	1:A:241:GLU:HG3	2.09	0.52
1:F:263:TYR:O	1:F:347:LEU:HD23	2.08	0.52
1:B:163:PRO:HG3	1:F:122:ASN:HD21	1.75	0.52
1:D:74:PHE:HB3	1:D:107:LEU:HD23	1.92	0.52
1:A:239:HIS:NE2	3:A:431:SO4:O1	2.42	0.52
1:C:321:CYS:HB3	1:C:327:ILE:HG12	1.92	0.52
1:B:58:VAL:HG12	1:B:59:ILE:N	2.24	0.52
1:C:40:LYS:HE3	1:D:226:ASN:ND2	2.18	0.52
1:C:224:ALA:HB3	1:C:225:PHE:CD1	2.44	0.52
1:E:226:ASN:HD21	1:F:40:LYS:HE2	1.74	0.52
1:F:262:ASP:O	1:F:263:TYR:HB2	2.10	0.52
1:E:164:ASN:H	1:E:164:ASN:ND2	2.03	0.52
1:B:86:VAL:HG12	1:B:86:VAL:O	2.10	0.51
1:B:369:GLU:OE1	3:B:431:SO4:O4	2.27	0.51
1:D:233:LYS:O	1:D:236:THR:HB	2.10	0.51
1:C:324:VAL:O	1:C:324:VAL:CG1	2.58	0.51
1:B:392:ASP:N	1:B:392:ASP:OD1	2.41	0.51
1:A:136:LYS:HZ1	1:D:136:LYS:NZ	2.08	0.51
1:B:135:TRP:CZ2	1:F:148:HIS:HD2	2.29	0.51
1:E:387:ILE:N	1:E:387:ILE:CD1	2.73	0.51
1:E:230:ALA:HB2	1:E:240:TYR:CD2	2.45	0.51
1:A:203:MSE:HG2	1:A:205:TYR:CZ	2.46	0.51
1:B:350:HIS:NE2	3:B:430:SO4:O2	2.44	0.51
1:C:164:ASN:HD22	1:C:164:ASN:N	2.07	0.51
1:D:148:HIS:CD2	1:F:135:TRP:CZ2	2.99	0.51
1:A:136:LYS:NZ	1:D:136:LYS:HZ1	2.09	0.51
1:E:1:MSE:HE2	1:E:179:ILE:HD12	1.91	0.51
1:C:40:LYS:CE	1:D:226:ASN:ND2	2.74	0.51
1:C:254:LEU:C	1:C:254:LEU:HD23	2.31	0.51
1:A:255:LEU:O	1:A:269:SER:HA	2.11	0.51
1:E:213:PHE:O	1:E:217:SER:OG	2.28	0.51
1:B:321:CYS:HB3	1:B:327:ILE:HG12	1.94	0.50
1:C:14:VAL:CG1	1:C:64:LYS:HE3	2.40	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:14:VAL:CG1	1:E:64:LYS:HE3	2.41	0.50
1:E:177:ILE:HD13	1:E:388:LEU:HD22	1.93	0.50
1:B:58:VAL:CG1	1:B:59:ILE:N	2.74	0.50
1:B:136:LYS:HZ1	1:E:136:LYS:HZ2	1.60	0.50
1:B:228:ILE:HB	1:B:256:ASP:HB3	1.93	0.50
1:E:392:ASP:N	1:E:392:ASP:OD1	2.44	0.50
1:B:412:MSE:O	1:B:416:ASN:HB3	2.11	0.50
1:C:226:ASN:ND2	1:D:40:LYS:HE2	2.27	0.50
1:D:1:MSE:CE	1:D:179:ILE:HD12	2.21	0.50
1:D:262:ASP:O	1:D:263:TYR:HB2	2.12	0.50
1:D:14:VAL:O	1:D:64:LYS:HE3	2.11	0.50
1:E:230:ALA:HB2	1:E:240:TYR:HD2	1.76	0.50
1:F:58:VAL:HG12	1:F:59:ILE:N	2.27	0.50
1:D:86:VAL:HG12	1:D:86:VAL:O	2.11	0.50
1:F:86:VAL:HG12	1:F:86:VAL:O	2.12	0.50
1:A:61:MSE:HE1	1:A:114:MSE:HE3	1.89	0.50
1:D:368:ILE:O	1:D:384:GLU:HA	2.12	0.50
1:B:194:VAL:HG13	1:B:207:LEU:HD22	1.93	0.50
1:C:248:GLN:O	1:C:251:ASP:HB2	2.12	0.50
1:C:368:ILE:O	1:C:384:GLU:HA	2.12	0.50
1:A:20:GLU:HA	1:A:65:PHE:CD1	2.47	0.49
1:B:369:GLU:HB3	1:B:384:GLU:CG	2.42	0.49
1:F:237:VAL:HB	1:F:240:TYR:HB2	1.94	0.49
1:D:418:ASN:ND2	1:D:418:ASN:N	2.60	0.49
1:B:135:TRP:CH2	1:F:148:HIS:HD2	2.29	0.49
1:C:416:ASN:OD1	1:C:418:ASN:ND2	2.45	0.49
1:E:61:MSE:CE	1:E:114:MSE:CE	2.72	0.49
1:B:248:GLN:O	1:B:251:ASP:HB2	2.12	0.49
1:C:163:PRO:HG3	1:E:122:ASN:ND2	2.28	0.49
1:E:129:ASP:OD1	1:E:129:ASP:C	2.51	0.49
1:F:404:GLU:HB2	1:F:407:GLU:HG3	1.94	0.49
1:E:295:GLU:O	1:E:298:GLU:HB3	2.12	0.49
1:F:418:ASN:ND2	1:F:418:ASN:H	2.10	0.49
1:D:148:HIS:HD2	1:F:135:TRP:CZ2	2.30	0.49
1:D:412:MSE:O	1:D:416:ASN:HB3	2.13	0.49
1:B:164:ASN:H	1:B:164:ASN:ND2	2.08	0.49
1:C:135:TRP:CZ2	1:E:148:HIS:HD2	2.31	0.49
1:C:341:VAL:O	1:C:369:GLU:HG2	2.13	0.49
1:F:295:GLU:O	1:F:298:GLU:HB3	2.13	0.49
1:D:58:VAL:HG12	1:D:59:ILE:N	2.27	0.49
1:B:164:ASN:O	1:B:168:LEU:HD13	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:ASN:HD21	1:D:163:PRO:HG3	1.78	0.48
1:D:255:LEU:O	1:D:269:SER:HA	2.13	0.48
1:E:58:VAL:HG13	1:E:74:PHE:O	2.13	0.48
1:B:368:ILE:O	1:B:384:GLU:HA	2.13	0.48
1:A:86:VAL:HG12	1:A:86:VAL:O	2.12	0.48
1:A:237:VAL:HB	1:A:240:TYR:HB2	1.94	0.48
1:D:164:ASN:HD22	1:D:164:ASN:N	2.12	0.48
1:E:175:GLU:H	1:E:175:GLU:CD	2.17	0.48
1:E:248:GLN:O	1:E:251:ASP:HB2	2.12	0.48
1:B:239:HIS:O	1:B:241:GLU:HG3	2.13	0.48
1:F:412:MSE:O	1:F:416:ASN:HB3	2.13	0.48
1:A:321:CYS:HB3	1:A:327:ILE:HG12	1.96	0.48
1:F:164:ASN:HD22	1:F:164:ASN:H	1.60	0.48
1:F:94:GLU:O	1:F:98:ILE:HG13	2.13	0.47
1:A:1:MSE:HG2	1:A:179:ILE:HD11	1.95	0.47
1:A:164:ASN:HD22	1:A:164:ASN:N	2.08	0.47
1:A:376:GLU:OE1	1:A:376:GLU:N	2.40	0.47
1:D:369:GLU:OE1	3:D:431:SO4:O2	2.31	0.47
1:B:418:ASN:ND2	1:B:418:ASN:H	2.13	0.47
1:C:175:GLU:CD	1:C:175:GLU:H	2.17	0.47
1:E:194:VAL:HG13	1:E:207:LEU:HD22	1.96	0.47
1:B:136:LYS:NZ	1:E:136:LYS:NZ	2.62	0.47
1:E:227:THR:HG23	1:E:257:LEU:HB3	1.97	0.47
1:F:410:GLU:OE2	1:F:414:GLU:OE1	2.33	0.47
1:E:56:PRO:O	1:E:57:ASN:HB2	2.15	0.47
1:E:172:LYS:HA	1:E:176:GLU:OE2	2.14	0.47
1:E:58:VAL:HG12	1:E:59:ILE:N	2.29	0.47
1:E:386:ASP:C	1:E:387:ILE:HD13	2.35	0.47
1:C:139:GLU:HG3	1:E:151[B]:GLU:OE2	2.15	0.47
1:E:1:MSE:HE1	1:E:176:GLU:HA	1.97	0.47
1:B:86:VAL:O	1:B:86:VAL:CG1	2.63	0.46
1:E:278:PHE:CD2	1:E:405:VAL:HG13	2.49	0.46
1:F:175:GLU:CD	1:F:175:GLU:H	2.17	0.46
1:F:278:PHE:CD2	1:F:405:VAL:HG13	2.49	0.46
1:F:369:GLU:CB	1:F:384:GLU:HB2	2.43	0.46
1:A:58:VAL:HG12	1:A:59:ILE:N	2.30	0.46
1:C:85:TRP:HA	1:D:238:LEU:HB2	1.97	0.46
1:E:112:LYS:HB3	1:E:112:LYS:HE3	1.58	0.46
1:D:122:ASN:ND2	1:F:163:PRO:HG3	2.31	0.46
1:D:297:THR:HG23	1:D:387:ILE:HG13	1.97	0.46
1:F:272:PHE:HB2	1:F:273:PRO:HD2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:135:TRP:CH2	1:E:148:HIS:HD2	2.33	0.46
1:C:255:LEU:O	1:C:269:SER:HA	2.16	0.46
1:B:254:LEU:C	1:B:254:LEU:CD2	2.84	0.46
1:F:248:GLN:O	1:F:251:ASP:HB2	2.15	0.46
1:F:56:PRO:O	1:F:57:ASN:HB2	2.16	0.46
1:B:122:ASN:ND2	1:D:163:PRO:HG3	2.31	0.46
1:F:86:VAL:O	1:F:86:VAL:CG1	2.64	0.46
1:A:392:ASP:OD1	1:A:392:ASP:N	2.49	0.45
1:D:252:LEU:HD12	1:D:273:PRO:HA	1.98	0.45
1:B:254:LEU:HD23	1:B:255:LEU:N	2.31	0.45
1:D:222:HIS:HA	3:D:433:SO4:O2	2.16	0.45
1:E:255:LEU:O	1:E:269:SER:HA	2.16	0.45
1:F:368:ILE:O	1:F:384:GLU:HA	2.17	0.45
1:A:122:ASN:HD21	1:E:163:PRO:HG3	1.82	0.45
1:A:86:VAL:O	1:A:86:VAL:CG1	2.64	0.45
1:D:196:LYS:O	1:D:196:LYS:HG3	2.16	0.45
1:B:324:VAL:O	1:B:324:VAL:HG12	2.17	0.45
1:D:404:GLU:HB2	1:D:407:GLU:HG3	1.97	0.45
1:D:279:SER:N	1:D:282:GLN:HE21	2.01	0.45
1:C:176:GLU:HG2	1:C:264:TYR:OH	2.17	0.45
1:A:56:PRO:O	1:A:57:ASN:HB2	2.17	0.44
1:D:29:GLN:HE21	1:D:141:LYS:HD2	1.71	0.44
1:C:178:GLU:O	1:C:181:LYS:HB2	2.17	0.44
1:D:148:HIS:CD2	1:F:135:TRP:CH2	2.97	0.44
1:F:254:LEU:C	1:F:254:LEU:HD23	2.38	0.44
1:A:1:MSE:HE1	1:A:176:GLU:HA	2.00	0.44
1:D:122:ASN:HD21	1:F:163:PRO:HG3	1.81	0.44
1:F:269:SER:HB2	1:F:384:GLU:HB3	1.98	0.44
1:B:255:LEU:O	1:B:269:SER:HA	2.18	0.44
1:E:26:PHE:CD1	1:E:59:ILE:HG12	2.52	0.44
1:E:172:LYS:HG3	1:E:365:VAL:CG2	2.47	0.44
1:F:324:VAL:O	1:F:324:VAL:CG1	2.65	0.44
1:A:112:LYS:HB3	1:A:112:LYS:HE3	1.65	0.44
1:A:164:ASN:H	1:A:164:ASN:ND2	2.09	0.44
1:C:164:ASN:H	1:C:164:ASN:ND2	2.08	0.44
1:E:74:PHE:HB3	1:E:107:LEU:HD23	1.99	0.44
1:C:233:LYS:O	1:C:236:THR:HB	2.18	0.44
1:B:141:LYS:HB3	1:B:141:LYS:HE2	1.65	0.44
1:B:233:LYS:O	1:B:236:THR:HB	2.18	0.44
1:E:290:LEU:O	1:E:293:LEU:HB3	2.17	0.44
1:F:252:LEU:HD12	1:F:252:LEU:HA	1.86	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:MSE:HE2	1:B:37:ALA:HB1	2.00	0.43
1:D:321:CYS:HB3	1:D:327:ILE:HG12	1.99	0.43
1:E:254:LEU:C	1:E:254:LEU:CD2	2.85	0.43
1:B:196:LYS:O	1:B:196:LYS:HG3	2.17	0.43
1:C:1:MSE:HE1	1:C:176:GLU:HA	2.00	0.43
1:D:224:ALA:HB3	1:D:225:PHE:CD1	2.53	0.43
1:E:162:TYR:N	1:E:163:PRO:CD	2.81	0.43
1:D:177:ILE:HD13	1:D:388:LEU:HD22	1.99	0.43
1:E:252:LEU:HD12	1:E:252:LEU:HA	1.86	0.43
1:E:396:ASN:OD1	1:E:396:ASN:C	2.56	0.43
1:A:14:VAL:HG13	1:A:64:LYS:CE	2.47	0.43
1:A:368:ILE:O	1:A:384:GLU:HA	2.18	0.43
1:D:203:MSE:HG2	1:D:205:TYR:OH	2.18	0.43
1:D:86:VAL:O	1:D:86:VAL:CG1	2.67	0.43
1:F:61:MSE:CE	1:F:114:MSE:HE3	2.44	0.43
1:F:255:LEU:O	1:F:269:SER:HA	2.19	0.43
1:A:233:LYS:O	1:A:236:THR:HB	2.19	0.43
1:F:112:LYS:HE3	1:F:112:LYS:HB3	1.78	0.43
1:F:249:ASN:ND2	1:F:275:ASN:HD22	2.16	0.43
1:B:177:ILE:HD13	1:B:388:LEU:HD22	2.01	0.43
1:D:10:ARG:O	1:D:14:VAL:HG23	2.19	0.43
1:E:398:SER:HB2	1:E:401:ILE:HD12	2.01	0.43
1:F:281:ARG:HH12	1:F:324:VAL:HG13	1.84	0.43
1:B:207:LEU:HD23	1:B:207:LEU:HA	1.84	0.43
1:C:136:LYS:NZ	1:F:136:LYS:NZ	2.66	0.43
1:D:392:ASP:OD1	1:D:392:ASP:N	2.52	0.42
1:F:194:VAL:HG13	1:F:207:LEU:HD22	2.00	0.42
1:A:167:GLU:OE1	1:A:167:GLU:HA	2.18	0.42
1:A:224:ALA:HB3	1:A:225:PHE:CD1	2.54	0.42
1:D:57:ASN:O	1:D:107:LEU:HD11	2.19	0.42
1:D:285:ILE:HG22	1:D:381:ILE:HD12	2.01	0.42
1:E:261:LYS:O	1:E:262:ASP:C	2.57	0.42
1:F:176:GLU:HG2	1:F:264:TYR:OH	2.19	0.42
1:C:94:GLU:O	1:C:98:ILE:HG13	2.19	0.42
1:C:164:ASN:N	1:C:164:ASN:ND2	2.67	0.42
1:E:369:GLU:HB3	1:E:384:GLU:HG3	2.00	0.42
1:A:40:LYS:HE2	1:B:226:ASN:HD21	1.85	0.42
1:B:387:ILE:HD12	1:B:396:ASN:HA	2.00	0.42
1:D:162:TYR:N	1:D:163:PRO:CD	2.83	0.42
1:F:386:ASP:C	1:F:387:ILE:HD13	2.40	0.42
1:F:224:ALA:HB3	1:F:225:PHE:CD1	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:GLU:OE2	1:A:414:GLU:OE1	2.37	0.42
1:E:229:LEU:HG	1:E:255:LEU:CD2	2.49	0.42
1:F:152:GLN:HA	1:F:152:GLN:NE2	2.34	0.42
1:F:203:MSE:HG2	1:F:205:TYR:OH	2.20	0.42
1:B:57:ASN:O	1:B:107:LEU:HD11	2.20	0.42
1:B:386:ASP:C	1:B:387:ILE:HD13	2.40	0.42
1:D:62:LEU:HD23	1:D:62:LEU:O	2.20	0.42
1:B:225:PHE:CZ	1:B:257:LEU:CA	3.02	0.42
1:C:56:PRO:O	1:C:57:ASN:HB2	2.19	0.42
1:C:172:LYS:HG3	1:C:365:VAL:HG23	2.02	0.42
1:B:136:LYS:HZ1	1:E:136:LYS:NZ	2.17	0.42
1:B:227:THR:HG23	1:B:257:LEU:HB3	2.02	0.42
1:C:1:MSE:CE	1:C:179:ILE:HD12	2.35	0.42
1:D:187:THR:O	1:D:191:ILE:HG13	2.20	0.42
1:C:86:VAL:O	1:C:86:VAL:CG1	2.68	0.41
1:D:112:LYS:HE3	1:D:112:LYS:HB3	1.77	0.41
1:E:153:TYR:HB3	1:E:156:VAL:HG23	2.02	0.41
1:C:68:SER:O	1:C:69:VAL:HG23	2.20	0.41
1:C:152:GLN:NE2	1:C:152:GLN:HA	2.36	0.41
1:C:163:PRO:HG3	1:E:122:ASN:HD21	1.85	0.41
1:E:254:LEU:HD23	1:E:255:LEU:N	2.34	0.41
1:B:148:HIS:CD2	1:D:135:TRP:CZ2	3.08	0.41
1:D:300:ILE:HD13	1:D:366:ILE:HD11	2.01	0.41
1:E:68:SER:O	1:E:69:VAL:HG23	2.20	0.41
1:B:261:LYS:O	1:B:262:ASP:C	2.57	0.41
1:C:230:ALA:HB2	1:C:240:TYR:CD2	2.56	0.41
1:F:176:GLU:HG2	1:F:264:TYR:CZ	2.56	0.41
1:C:86:VAL:O	1:C:86:VAL:HG12	2.20	0.41
1:A:194:VAL:HG13	1:A:207:LEU:HD22	2.03	0.41
1:B:110:PHE:CE1	1:B:114:MSE:HE3	2.56	0.41
1:B:136:LYS:HZ3	1:E:136:LYS:HZ1	1.69	0.41
1:E:322:LYS:NZ	1:E:330:ASP:OD1	2.26	0.41
1:B:269:SER:H	1:B:384:GLU:HB3	1.86	0.41
1:B:322:LYS:NZ	1:B:330:ASP:OD1	2.32	0.41
1:C:20:GLU:HA	1:C:65:PHE:CD1	2.56	0.41
1:D:248:GLN:O	1:D:251:ASP:HB2	2.21	0.41
1:E:164:ASN:ND2	1:E:164:ASN:N	2.67	0.41
1:E:321:CYS:CB	1:E:327:ILE:HG12	2.46	0.41
1:E:369:GLU:HB3	1:E:384:GLU:CG	2.51	0.41
1:E:410:GLU:OE2	1:E:414:GLU:OE1	2.38	0.41
1:F:12:ARG:CB	1:F:168:LEU:CD2	2.99	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:PHE:O	1:B:68:SER:HB2	2.21	0.41
1:B:135:TRP:CE3	1:F:153:TYR:HE2	2.39	0.41
1:C:135:TRP:CZ2	1:E:148:HIS:CD2	3.09	0.41
1:D:148:HIS:HD2	1:F:135:TRP:CZ3	2.39	0.41
1:C:369:GLU:HB3	1:C:384:GLU:HB2	2.04	0.40
1:C:411:PHE:CD2	1:C:411:PHE:C	2.94	0.40
1:C:147:LYS:HE3	1:C:151:GLU:OE2	2.21	0.40
1:C:324:VAL:O	1:C:324:VAL:HG12	2.21	0.40
1:D:14:VAL:HG13	1:D:64:LYS:HE3	2.03	0.40
1:A:322:LYS:NZ	1:A:330:ASP:OD1	2.43	0.40
1:E:108:ASP:OD1	1:E:108:ASP:C	2.60	0.40
1:B:288:ILE:HG23	1:B:320:GLY:HA3	2.03	0.40
1:C:199:LYS:HD3	1:C:418:ASN:OD1	2.22	0.40
1:D:369:GLU:HB3	1:D:384:GLU:CG	2.52	0.40
1:B:1:MSE:HE1	1:B:176:GLU:HA	2.03	0.40
1:B:129:ASP:OD1	1:B:129:ASP:C	2.59	0.40
1:C:272:PHE:HB2	1:C:273:PRO:HD2	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	418/427 (98%)	406 (97%)	11 (3%)	1 (0%)	47 78
1	B	418/427 (98%)	402 (96%)	16 (4%)	0	100 100
1	C	418/427 (98%)	401 (96%)	17 (4%)	0	100 100
1	D	419/427 (98%)	404 (96%)	15 (4%)	0	100 100
1	E	418/427 (98%)	393 (94%)	25 (6%)	0	100 100
1	F	419/427 (98%)	400 (96%)	18 (4%)	1 (0%)	47 78
All	All	2510/2562 (98%)	2406 (96%)	102 (4%)	2 (0%)	51 82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	417	VAL
1	A	417	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	371/369 (100%)	366 (99%)	5 (1%)	69	90
1	B	371/369 (100%)	364 (98%)	7 (2%)	57	84
1	C	371/369 (100%)	366 (99%)	5 (1%)	69	90
1	D	372/369 (101%)	365 (98%)	7 (2%)	57	84
1	E	371/369 (100%)	361 (97%)	10 (3%)	44	77
1	F	372/369 (101%)	366 (98%)	6 (2%)	62	86
All	All	2228/2214 (101%)	2188 (98%)	40 (2%)	59	85

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	62	LEU
1	A	238	LEU
1	A	257	LEU
1	A	418	ASN
1	B	62	LEU
1	B	217	SER
1	B	238	LEU
1	B	257	LEU
1	B	315	LYS
1	B	360	LEU
1	B	418	ASN
1	C	2	LYS
1	C	62	LEU
1	C	164	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	257	LEU
1	C	418	ASN
1	D	2	LYS
1	D	29	GLN
1	D	238	LEU
1	D	257	LEU
1	D	387	ILE
1	D	417	VAL
1	D	418	ASN
1	E	29	GLN
1	E	164	ASN
1	E	175	GLU
1	E	217	SER
1	E	257	LEU
1	E	324	VAL
1	E	338	TYR
1	E	387	ILE
1	E	391	LYS
1	E	418	ASN
1	F	1	MSE
1	F	2	LYS
1	F	238	LEU
1	F	257	LEU
1	F	324	VAL
1	F	418	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	32	HIS
1	A	38	HIS
1	A	57	ASN
1	A	122	ASN
1	A	148	HIS
1	A	152	GLN
1	A	164	ASN
1	A	193	ASN
1	A	226	ASN
1	A	248	GLN
1	A	282	GLN
1	A	310	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	418	ASN
1	B	116	ASN
1	B	122	ASN
1	B	148	HIS
1	B	164	ASN
1	B	193	ASN
1	B	226	ASN
1	B	248	GLN
1	B	249	ASN
1	B	282	GLN
1	B	310	ASN
1	B	418	ASN
1	C	29	GLN
1	C	116	ASN
1	C	122	ASN
1	C	148	HIS
1	C	152	GLN
1	C	164	ASN
1	C	193	ASN
1	C	226	ASN
1	C	248	GLN
1	C	249	ASN
1	C	260	GLN
1	C	282	GLN
1	C	310	ASN
1	C	418	ASN
1	D	29	GLN
1	D	116	ASN
1	D	122	ASN
1	D	148	HIS
1	D	164	ASN
1	D	193	ASN
1	D	226	ASN
1	D	234	ASN
1	D	248	GLN
1	D	249	ASN
1	D	260	GLN
1	D	282	GLN
1	D	310	ASN
1	D	418	ASN
1	E	29	GLN
1	E	116	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	122	ASN
1	E	148	HIS
1	E	152	GLN
1	E	164	ASN
1	E	193	ASN
1	E	226	ASN
1	E	248	GLN
1	E	282	GLN
1	E	310	ASN
1	E	418	ASN
1	F	29	GLN
1	F	116	ASN
1	F	122	ASN
1	F	148	HIS
1	F	152	GLN
1	F	164	ASN
1	F	193	ASN
1	F	226	ASN
1	F	248	GLN
1	F	249	ASN
1	F	282	GLN
1	F	310	ASN
1	F	418	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 51 ligands modelled in this entry, 12 are monoatomic - leaving 39 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	432	-	4,4,4	0.21	0	6,6,6	0.20	0
3	SO4	A	430	-	4,4,4	0.26	0	6,6,6	0.08	0
3	SO4	A	436[A]	-	4,4,4	0.27	0	6,6,6	0.15	0
3	SO4	B	433	-	4,4,4	0.29	0	6,6,6	0.23	0
3	SO4	F	431	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	C	435	-	4,4,4	0.31	0	6,6,6	0.31	0
3	SO4	F	430	2	4,4,4	0.26	0	6,6,6	0.09	0
3	SO4	F	432	-	4,4,4	0.28	0	6,6,6	0.15	0
3	SO4	C	430	2	4,4,4	0.26	0	6,6,6	0.18	0
3	SO4	B	432	-	4,4,4	0.25	0	6,6,6	0.36	0
3	SO4	C	434	-	4,4,4	0.29	0	6,6,6	0.39	0
3	SO4	A	433	-	4,4,4	0.25	0	6,6,6	0.08	0
3	SO4	E	430	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	A	436[B]	-	4,4,4	0.26	0	6,6,6	0.12	0
3	SO4	A	435	-	4,4,4	0.27	0	6,6,6	0.24	0
3	SO4	D	434	-	4,4,4	0.24	0	6,6,6	0.23	0
3	SO4	F	433	-	4,4,4	0.29	0	6,6,6	0.14	0
3	SO4	C	432	-	4,4,4	0.29	0	6,6,6	0.11	0
3	SO4	C	433	-	4,4,4	0.26	0	6,6,6	0.13	0
3	SO4	E	431	-	4,4,4	0.27	0	6,6,6	0.13	0
3	SO4	A	431	-	4,4,4	0.24	0	6,6,6	0.23	0
3	SO4	A	434	-	4,4,4	0.28	0	6,6,6	0.11	0
3	SO4	B	430	-	4,4,4	0.25	0	6,6,6	0.12	0
3	SO4	E	432	-	4,4,4	0.26	0	6,6,6	0.25	0
3	SO4	D	432	-	4,4,4	0.27	0	6,6,6	0.22	0
3	SO4	B	431	-	4,4,4	0.27	0	6,6,6	0.15	0
3	SO4	D	430	-	4,4,4	0.25	0	6,6,6	0.18	0
3	SO4	D	433	-	4,4,4	0.29	0	6,6,6	0.14	0
3	SO4	E	434	-	4,4,4	0.26	0	6,6,6	0.14	0
3	SO4	F	435	-	4,4,4	0.29	0	6,6,6	0.20	0
3	SO4	F	434	-	4,4,4	0.30	0	6,6,6	0.31	0
3	SO4	B	435	-	4,4,4	0.27	0	6,6,6	0.53	0
3	SO4	B	434	-	4,4,4	0.29	0	6,6,6	0.12	0
3	SO4	D	431	-	4,4,4	0.25	0	6,6,6	0.15	0
3	SO4	D	435	-	4,4,4	0.27	0	6,6,6	0.23	0
3	SO4	D	436	-	4,4,4	0.28	0	6,6,6	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	E	433	-	4,4,4	0.25	0	6,6,6	0.20	0
3	SO4	C	431	-	4,4,4	0.26	0	6,6,6	0.21	0
3	SO4	A	437	-	4,4,4	0.30	0	6,6,6	0.41	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	430	SO4	2	0
3	F	430	SO4	1	0
3	F	433	SO4	1	0
3	C	433	SO4	1	0
3	A	431	SO4	1	0
3	B	430	SO4	1	0
3	B	431	SO4	1	0
3	D	433	SO4	1	0
3	D	431	SO4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	410/427 (96%)	-0.12	3 (0%)	87	87	28, 43, 72, 98	0
1	B	410/427 (96%)	-0.09	2 (0%)	91	91	28, 43, 72, 98	0
1	C	410/427 (96%)	-0.03	3 (0%)	87	87	28, 43, 72, 98	0
1	D	410/427 (96%)	-0.20	2 (0%)	91	91	28, 43, 72, 98	0
1	E	410/427 (96%)	0.19	21 (5%)	28	24	28, 43, 72, 98	0
1	F	410/427 (96%)	-0.01	7 (1%)	70	69	28, 43, 72, 98	0
All	All	2460/2562 (96%)	-0.04	38 (1%)	73	73	28, 43, 73, 98	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	419	VAL	4.9
1	E	419	VAL	4.6
1	E	285	ILE	4.4
1	E	418	ASN	4.3
1	E	328	GLN	4.0
1	E	327	ILE	3.7
1	B	417	VAL	3.6
1	A	418	ASN	3.4
1	F	328	GLN	3.1
1	E	334	SER	3.0
1	E	319	GLU	2.9
1	E	324	VAL	2.9
1	F	419	VAL	2.9
1	F	67	ASN	2.8
1	E	326	LEU	2.8
1	E	67	ASN	2.8
1	E	323	ALA	2.8
1	B	93	GLU	2.6
1	E	336	TYR	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	4	LYS	2.6
1	C	233	LYS	2.5
1	E	417	VAL	2.5
1	E	416	ASN	2.4
1	F	417	VAL	2.4
1	F	418	ASN	2.4
1	F	79	ASP	2.3
1	E	332	GLU	2.3
1	C	102	LYS	2.3
1	F	327	ILE	2.3
1	E	330	ASP	2.2
1	E	288	ILE	2.2
1	E	299	ILE	2.2
1	E	391	LYS	2.1
1	E	320	GLY	2.1
1	C	392	ASP	2.1
1	D	331	GLU	2.1
1	A	93	GLU	2.0
1	A	413	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	D	436	5/5	0.76	0.33	34,39,51,54	5
3	SO4	C	435	5/5	0.80	0.31	40,50,61,63	5
3	SO4	B	435	5/5	0.82	0.30	43,46,54,55	5
3	SO4	C	431	5/5	0.83	0.35	62,64,70,70	5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	D	430	5/5	0.84	0.31	64,66,74,74	5
3	SO4	F	431	5/5	0.85	0.43	77,78,85,85	5
3	SO4	E	431	5/5	0.86	0.30	64,68,72,72	5
3	SO4	F	430	5/5	0.86	0.34	78,79,81,81	5
3	SO4	A	437	5/5	0.86	0.35	32,35,42,48	5
3	SO4	F	435	5/5	0.86	0.23	55,58,61,62	5
3	SO4	B	431	5/5	0.87	0.30	76,76,78,80	5
3	SO4	A	431	5/5	0.87	0.46	61,66,70,71	5
3	SO4	C	430	5/5	0.88	0.27	68,70,76,76	5
3	SO4	D	431	5/5	0.89	0.30	70,73,74,78	5
3	SO4	A	434	5/5	0.90	0.27	57,61,62,65	5
3	SO4	A	435	5/5	0.90	0.19	53,57,62,64	5
3	SO4	E	434	5/5	0.90	0.22	57,61,63,67	5
3	SO4	A	436[B]	5/5	0.91	0.26	62,64,66,69	5
3	SO4	B	434	5/5	0.91	0.24	45,50,53,59	5
3	SO4	C	433	5/5	0.91	0.78	53,55,59,62	5
3	SO4	A	436[A]	5/5	0.91	0.26	55,58,59,62	5
3	SO4	F	433	5/5	0.92	0.73	42,43,48,51	5
3	SO4	E	430	5/5	0.92	0.24	76,76,81,83	5
3	SO4	E	433	5/5	0.93	0.75	54,55,56,61	5
3	SO4	B	433	5/5	0.93	0.52	44,45,47,54	5
3	SO4	B	430	5/5	0.93	0.27	63,64,69,70	5
2	MN	C	429	1/1	0.94	0.04	138,138,138,138	0
3	SO4	D	433	5/5	0.94	0.55	48,48,50,53	5
3	SO4	D	435	5/5	0.94	0.17	37,37,45,45	5
3	SO4	F	434	5/5	0.94	0.26	40,44,49,51	5
3	SO4	A	430	5/5	0.94	0.37	76,77,80,81	5
2	MN	A	429	1/1	0.95	0.12	126,126,126,126	0
3	SO4	A	433	5/5	0.95	0.69	47,50,54,56	5
2	MN	C	428	1/1	0.95	0.08	97,97,97,97	0
2	MN	F	429	1/1	0.96	0.06	118,118,118,118	0
2	MN	E	428	1/1	0.96	0.09	100,100,100,100	0
3	SO4	C	434	5/5	0.97	0.10	66,67,70,71	0
3	SO4	F	432	5/5	0.97	0.21	76,80,83,85	0
3	SO4	A	432	5/5	0.97	0.12	64,65,66,67	0
2	MN	E	429	1/1	0.97	0.08	149,149,149,149	0
2	MN	D	429	1/1	0.97	0.08	125,125,125,125	0
3	SO4	D	434	5/5	0.98	0.10	57,62,67,70	0
2	MN	F	428	1/1	0.98	0.10	87,87,87,87	0
3	SO4	C	432	5/5	0.98	0.15	77,79,81,82	0
3	SO4	B	432	5/5	0.98	0.10	56,64,69,75	0
3	SO4	D	432	5/5	0.98	0.11	60,61,64,71	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	E	432	5/5	0.98	0.10	65,69,72,77	0
2	MN	B	429	1/1	0.98	0.11	128,128,128,128	0
2	MN	D	428	1/1	0.99	0.08	78,78,78,78	0
2	MN	B	428	1/1	0.99	0.10	74,74,74,74	0
2	MN	A	428	1/1	0.99	0.10	75,75,75,75	0

6.5 Other polymers (i)

There are no such residues in this entry.